AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of the claims:

1. **(Currently Amended)** A method for screening a compound library to identify a compound with a physiological effect on a biological sample, the method comprising:

(a) contacting a plurality of biological samples with a plurality of members of a compound library;

(b) obtaining an expressed RNA sample from each of the plurality of biological samples;

(c) producing a plurality of nucleic acid samples from the plurality of expressed RNA samples, said nucleic acid samples selected from:

(i) total cellular RNA or a subset thereof isolated from said biological samples;

(ii) mRNA isolated from said biological samples;

(iii) cDNA produced from (i) or (ii); and

(iv) nucleic acids amplified from (i), (ii) or (iii);

and wherein each nucleic acid sample comprises a plurality of different nucleic acid species;

(d) arraying said plurality of nucleic acid samples to produce a nucleic acid array, wherein each sample is deposited at a single unique location on the array;

(e) hybridizing a plurality of defined sequence probes to said nucleic acid array, which probes each comprise a different polynucleotide sequence, and which probes are each capable of generating a different detectable signal;

(f) quantitating a signal corresponding to hybridization of each of the plurality of defined sequence probes to the nucleic acid array, thereby generating a quantitated hybridization signal; and,

(g) detecting at least one quantitated hybridization signal that differs from a control hybridization signal, thereby identifying a compound that exerts a physiological effect on a biological sample; and,

(h) entering the quantitated hybridization signal into a database.

2. (Original) The method of claim **1**, wherein each of the plurality of biological samples is contacted with a different member of the compound library.

3. (Original) The method of claim **1**, wherein the control hybridization signal is produced by:

(i) providing a nucleic acid array comprising a plurality of control nucleic acids obtained from a control biological sample;

(ii) hybridizing the plurality of defined sequence probes to the nucleic acid array comprising the control nucleic acids; and,

(iii) detecting a control hybridization signal.

4. (Original) The method of claim **3**, wherein the control nucleic acids comprise amplification products.

5. (Previously Presented) The method of claim **3**, wherein the control biological sample comprises an untreated biological sample or a 0 time point sample.

6. (Original) The method of claim **1**, wherein the quantitated hybridization signal differs qualitatively or quantitatively relative to the control hybridization signal.

7. (Original) The method of claim **1**, wherein the quantitated hybridization signal is increased or decreased relative to the control hybridization signal.

8. (Original) The method of claim **1**, comprising detecting the quantitated hybridization signal that differs from a control hybridization signal by performing at least one statistical analysis.

9. (Original) The method of claim **1**, wherein the quantitated hybridization signal is increased or decreased at least one standard deviation relative to the control hybridization signal.

10. (Original) The method of claim **1**, wherein the quantitated hybridization signal is increased or decreased at least two standard deviations relative to the control hybridization signal.

11. (Original) The method of claim **1**, comprising providing a plurality of nucleic acid arrays.

12. (Original) The method of claim **1**, wherein the biological samples comprise one or more of: a tissue, a tissue extract, a primary cell isolate and cells grown in culture.

13. (Original) The method of claim **1**, wherein the biological samples comprise one or more cell lines.

14. (Original) The method of claim **13**, wherein expression of one or more genes in the one or more cell lines is artificially altered prior to treating with a member of a compound library using a procedure selected from the group consisting of: insertional mutagenesis, deletion of genomic DNA, targeted gene disruption, transcription blocking, introduction of a genomic or episomal vector, antisense DNA or RNA, ribozymes, iRNA, DNA binding oligonucleotides, and zinc finger proteins.

15. (Original) The method of claim **1**, wherein the biological samples comprise eukaryotic samples.

16. (Original) The method of claim **1**, wherein the biological samples comprise prokaryotic samples.

17. (Original) The method of claim **1**, wherein the compound library comprises one or more of: a compound collection library, a combinatorial chemical library, a scaffold-focused chemical library, a target focused chemical library, an antibody library, a biological library, a natural product library, an antisense agent library, an iRNA library, a siRNA library, a ribozyme library, a peptide library, and a combinatorial nucleic acid oligomer library.

18. (Original) The method of claim **1**, comprising obtaining expressed RNA samples from at least 500 biological samples, each of which biological samples is treated with a different member of a compound library.

19. (Original) The method of claim **1**, comprising obtaining expressed RNA samples from at least 1000 biological samples, each of which biological samples is treated with a different member of a compound library.

20. (Original) The method of claim **1**, comprising obtaining expressed RNA samples from at least 10,000 biological samples, each of which biological samples is treated with a different member of a compound library.

21. (Original) The method of claim **1**, comprising obtaining the one or more expressed RNA samples by isolating total cellular RNA.

22. (Original) The method of claim **1**, comprising obtaining the one or more expressed RNA samples by isolating messenger RNA (mRNA).

23. (Cancelled)

24. (Previously Presented) The method of claim **1**, wherein said nucleic acid samples~~,~~ are produced by selective amplification of members of said expressed RNA samples, thereby producing selectively amplified nucleic acid samples.

25. (Currently Amended) A method for simultaneously quantitating a plurality of expression products from a plurality of biological samples, the method comprising:

(a) providing a plurality of biological samples;

(b) obtaining expressed RNA samples from said biological samples;

(c) amplifying a plurality of different members in said expressed RNA samples by selective amplification, thereby producing selectively amplified nucleic acid samples, said selectively amplified nucleic acid samples each comprising a plurality of amplified nucleic acid species;

(d) arraying a plurality of said selectively amplified nucleic acid samples to produce at least one nucleic acid array, wherein each sample is deposited at a single unique location on the array; and

(e) hybridizing a plurality of defined sequence probes to said nucleic acid array, which defined sequence probes each comprise a different polynucleotide

sequence, and which probes are each capable of generating a different detectable signal, to the nucleic acid array; and,

(f) detecting a signal corresponding to hybridization to each of the plurality of defined sequence probes.

26. (Previously Presented) The method of claim **24** or **25**, wherein the selectively amplified nucleic acid samples are produced by selective amplification by one or more method selected from the group consisting of: PCR, TMA, NASBA, and RCA.

27. (Original) The method of claim **24** or **25**, wherein the selective amplification is performed by PCR.

28. (Original) The method of claim **24** or **25**, wherein the selective amplification is performed by multiplex PCR using a plurality of gene specific primers.

29. (Original) The method of claim **28**, wherein the gene specific primers further comprise a universal priming sequence.

30. (Previously Presented) The method of claim **24** or **25**, wherein the products of said selective amplification are pooled for arraying.

31. (Original) The method of claim **24** or **25**, wherein the selective amplification amplifies between about 5 and about 100 polynucleotide sequences.

32. (Original) The method of claim **24** or **25**, wherein the selective amplification amplifies between about 10 and about 50 polynucleotide sequences.

33. (Original) The method of claim **24** or **25**, comprising amplifying each expressed RNA sample in two or more target specific amplification reactions and spatially arraying the resulting amplification products in two or more locations on an array.

34. (Original) The method of claim **33**, comprising hybridizing a plurality of probes each of which specifically hybridizes to the products of a different target specific amplification reaction.

35. (Previously Presented) The method of claim **1** or **25**, wherein the plurality of defined sequence probes comprises at least a first defined sequence probe and at least a

second defined sequence probe, which first defined sequence probe hybridizes to a housekeeping gene and which second defined sequence probe hybridizes to a target sequence; and wherein step (f) of claim **1** or step (f) of claim **25** further comprises determining the detectable signal of the second defined sequence probe relative to the detectable signal of the first defined sequence probe.

36. (Previously Presented) The method of claim **35**, wherein the nucleic acid samples corresponding to the expressed RNA samples are arrayed in two or more duplicate arrays, and each array is hybridized to the first defined sequence probe and the second defined sequence probe, wherein the first defined sequence probe is the same between the two or more duplicate arrays and the second defined sequence probe differs between the two or more duplicate arrays.

37. (Original) The method of claim **1** or **25**, wherein plurality of defined sequence probes comprises set of genes comprising disease related targets.

38. (Previously Presented) The method of claim **1** or **25**, comprising arraying the nucleic acid samples on a solid phase surface.

39. (Previously Presented) The method of claim **38**, comprising arraying the nucleic acid samples on a two dimensional solid phase surface.

40. (Previously Presented) The method of claim **38**, comprising arraying the nucleic acid samples on a plurality of solid phase surfaces.

41. (Original) The method of claim **40**, wherein the plurality of solid phase surfaces are selected from the group consisting of: beads, spheres and optical fibers.

42. (Original) The method of claim **38**, wherein the solid phase surface comprises a material selected from the group consisting of: glass, coated glass, silicon, porous silicon, nylon, ceramic and plastic.

43. (Original) The method of claim **1** or **25**, wherein the defined sequence probes comprise one or more synthetic probes selected from the group consisting of: an oligonucleotide, a cDNA; an amplification product, and a restriction fragment.

44. (Original) The method of claim **1** or **25**, wherein the defined sequence probes capable of generating a detectable signal comprise one or more of: a fluorescent label, a chromophore, an electrophore, a radioactive nuclide, a chemically reactive moiety, an amplifiable signal element and a ligand capable of binding to an enzyme.

45. (Original) The method of claim **44**, wherein the amplifiable signal element is an oligonucleotide.

46. (Original) The method of claim **45**, wherein at least one of the plurality of defined sequence probes comprising an amplifiable signal element is detected by one or more of branched DNA amplification (BDA), rolling circle amplification (RCA), hybridization signal amplification method (HSAM), ramification amplification method (RAM) and a DNA dendrimer probe.

47. (Previously Presented) The method of claim **44**, wherein at least one of the plurality of defined sequence probes comprises an amplifiable signal element, which amplifiable signal element comprises a ligand which binds to a second amplifiable signal element.

48. (Original) The method of claim **44**, wherein the amplifiable signal element comprises an enzyme or a catalyst.

49. (Previously Presented) The method of claim **1** or **25**, further comprising amplifying at least one detectable signal prior to detecting or quantitating a signal corresponding to hybridization.

50. (Previously Presented) The method of claim **1** or **25**, further comprising comparing the detected or quantitated signal corresponding to hybridization between samples.

51-57. (Cancelled)

58. (Currently Amended) A method of screening a compound library for an effect on an expression level in a biological sample, the method comprising:

a.) contacting a plurality of biological samples with a plurality of members of the compound library;

b.) obtaining an expressed RNA sample from each of the plurality of biological samples;

c.) producing a nucleic acid sample from each of the expressed RNA samples, wherein each nucleic acid sample comprises a plurality of different nucleic acid species;

d.) depositing the nucleic acid samples onto a solid phase array, wherein each sample is deposited at a single unique location on the array;

e.) hybridizing a plurality of solution based defined sequence probes to the array, wherein each of the defined sequence probes comprises a different detectable label; and,

f.) detecting a signal from each of the defined sequence probes and comparing the signal to a control signal, thereby identifying a compound that has an effect on an expression level in the biological sample.